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**FIG. 1 Promyostatin**

1	<u>MQKLQLCVYI</u>	<u>YL</u> FMLIVAGP	<u>VDLNENSEQK</u>	ENVEKEGLCN	40
41	ACTWRQNTKS	SRIEAIKIQI	LSKLRLETAP	NISKDVIRQL	80
81	LPKAPPLREL	IDQYDVQRDD	SSDGSLEDDD	YHATTETIIT	120
121	MPTESDFLMQ	VDGKPCCFF	KFSSKIQYNK	VVKAQLWIYL	160
161	RPVETPTTVF	VQILRLIKPM	KDGTRYTGIR	SLKLDMNP GT	200
201	GIWQSIDVKT	VLQNWLKQPE	SNLGIEIKAL	DENGHD LAVT	240
241	FPGPGEDGLN	PFLEVKVTD T	PKRSRRDFGL	DCDEHSTESR	280
281	CCRYPLTVDF	EA FGWDWIIA	PKRYKANYCS	GECEFVFLQK	320
321	YPHTHLVHQ A	NPRGSAGPCC	TPTKMSPINM	LYFNGKEQII	360
361	YGKIPAMVVD	RCGCS	376	(SEQ ID NO:1)	

**FIG. 2 Mature Myostatin (Human, murine, rat, chicken)**

1	DFGLDCDEHS	TESRCCRYPL	TVDFEAFGWD	WIAPKRYK <u>A</u>	40
41	<u>NYCSGECEFV</u>	<u>FLQKY</u> PHTHL	VHQANPRGSA	GPCCTPTKMS	80
81	PINMLYFNGK	EQIIYGKIPA	MVVDR CGCS	109	(SEQ ID NO:2)

**FIG. 3 Myostatin Homology with GDF-11**

Myostatin	DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYK
Consensus	-+GLDCDEHS+ESRCCRYPLTVDFEAFGWDWIIAPKRYK
GDF-11	NLGLDCDEHSSES RCCRYPLTVDFEAFGWDWIIAPKRYK

Myostatin	ANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTK
Consensus	ANYCSG+CE++F+QKYPHTHLV-QANPRGSAGPCCTPTK
GDF-11	ANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTK

Myostatin	MSPINMLYFNGKEQIIYGKIPAMVVDR CGCS	109	(SEQ ID NO:2)
Consensus	MSPINMLYFN-K+QIIYGKIP+MV VDR CGCS		(SEQ ID NO:39)
GDF-11	MSPINMLYFNDKQQIIYGKIPGMVVDR CGCS	108	(SEQ ID NO:40)

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Figure 4 Fab Light Chain Variable Region Alignment

<u>FAb</u>	1	<u>CDR1</u>	40
3	QIVLTQSPA I	MSASPGEKVT	MTC SASSSIS YMHWYQQKPG
5	QVVL TQSPA I	MSASLGEKVT	MTC SASSSVH YMHWYQQKSG
7	QIVLTQSPA I	MSASPGEKVT	MTC SASSSIS YMHWYQQKPG
8	QIVLTQSPA I	MSASPGEKVT	MTC SASSSVS YMHWYQQKSG
9	QIVLTQSPA I	MSASPGEKVT	MTC SASSSVS YMHWYQQKSG
10	QVVL TQSPA I	MSASPGEKVT	MTC SASSSIS YMHWYQQKPG
11	QIVLTQSPA I	MSASPGEKVT	MTC SASSSIS YMHWYQQKPG
12	QVVL TQSPA I	MSASPGEKVT	MTC SASSSVY YMHWYQQRSG
14	QIVLTQSPA I	MSASPGEKVT	MTC SASSSVS YMHWYQQKPG
15	QIVLTQSPA I	MSASPGEEV T	MTC SASSSI N YMHWYQQKSG
	*	*	**
<u>FAb</u>	41	<u>CDR2</u>	80
3	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
5	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
7	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
8	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
9	TSPKRWIYDT	SKLASGPVR	FSGSGSGTSY SLTISSMEAE
10	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
11	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
12	ASPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
14	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
15	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY SLTISSMEAE
	*		
<u>FAb</u>	81	<u>CDR3</u>	108
3	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD (SEQ ID NO:3)
5	DAATYYCQQW	SSNPLTFGAG	TKLELKRAD (SEQ ID NO:4)
7	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD (SEQ ID NO:3)
8	DAATYYCQQW	SSNPLTFGAG	TKLELKRAD (SEQ ID NO:5)
9	DAATYYCQQW	SRNPLTFGAG	TKLELKRAD (SEQ ID NO:6)
10	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD (SEQ ID NO:7)
11	DAATYYCQQW	NSNPLTFGAG	TKLELKRAD (SEQ ID NO:8)
12	DAATYYCQQW	TYNPLTFGAG	TKLELKRAD (SEQ ID NO:9)
14	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD (SEQ ID NO:10)
15	DAATYYCQQW	NSNPLTFGGG	TKLELKRAD (SEQ ID NO:11)
	**	*	

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Figure 5 Fab Heavy Chain Variable Region Alignment  
FAb 1    CDR1                            40

3	QVTLKESGPG	ILQSSQTLSL	TCSLSGFSLR	TSGMSVSWIR
5	QVTLKESGPG	ILQSSQTLSL	TCSFSGFSLS	TSGMSVSWIR
7	QVTLK-SGPG	ILQSSQTLTL	TCSLSGFSLT	TSGMIVSWIR
8	QVTLKESGPG	ILQSSQTLSL	TCSLSGFSLR	TSGMSVSWIR
9	QVTLKESGPG	ILQSSQTLSL	TCSVSGFSLS	TSGMSVSWIR
10	QVTLKESGPG	ILQPSQTLSL	TCSLSGFSLR	TSGMSVSWIR
11	QVTLKESGPG	ILQSSQTLSL	TCSLSGFSLR	TSGMSVSWIR
12	QVTLKESGPG	MLQSSQTLSL	TCSLSGFSLR	TSGMSVSWIR
14	QVTLKESGPG	ILQSSQTLSL	TCSLSGFSLR	TSGMSVSWIR
15	QVTLKESGPG	ILQSSQTLSL	TCSLSGFSLR	TSGMSVSWIR
	*	*	*	*

<u>FAb</u>	41	<u>CDR2</u>		80
3	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
5	QSSGKGLEWL	AHIYWDDDKR	YNPSLRSRLT	ISKDTSRNQV
7	QSSGRGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
8	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
9	QPSGKGLEWL	AHIYWDDDKR	YNPSLKSRLT	ISKDTSRNQV
10	QSSGKGLEWL	AHIYWDDDR	YNPSLRNRLT	ISKDTLRNQV
11	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
12	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
14	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
15	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV
	*	*	**	*

<u>FAb</u>	81	<u>CDR3</u>		
3	FLKITSVGTADTATYYCARRAITT	VIGGGTMDYWGQGTSVTVSS		
5	FLKITSVDTADTATYYCARRGI	TTVLGGGTMDYWGQGTSVTVSS		
7	FLWISSVGTADTATYYCARRAIT	TVVIGGGTMDYWGQGTSVTVSS		
8	FLKITSVGTADTATYYCARRAIT	TVVIGGGTMDYWGQGTSVTVSS		
9	FLKITSVDTADTATYYCARRAIT	TVLGGGTMDYWGQGTSVTVSS		
10	FLKITSVGTADTATYYCARRAI	TTVIGGGTMDYWGQGTSVTVSS		
11	FLKITSVGTADTATYYCARRAIT	TVVIGGGTMDYWGQGTSVTVSS		
12	FLKITSVGTADTATYYCARRAIT	TVVIGGGTMDYWGQGTSVTVSS		
14	FLKITSVGTADTATYYCARRAIT	TVVIGGGTMDYWGQGTSVTVSS		
15	FLKITSVGTADTATYYCARRAIT	TVVIGGGTMDYWGQGTSVTVSS		
	*	*	*	*

3	(SEQ ID NO:12)
5	(SEQ ID NO:13)
7	(SEQ ID NO:14)
8	(SEQ ID NO:12)
9	(SEQ ID NO:15)
10	(SEQ ID NO:17)
11	(SEQ ID NO:12)
12	(SEQ ID NO:16)
14	(SEQ ID NO:12)
15	(SEQ ID NO:12)